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**TRANSMITTAL
FORM**

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Total Number of Pages in This Submission

27

Application Number

10/629,448

Filing Date

July 29, 2003

First Named Inventor

Kelkar et. al.

Art Unit

1631

Examiner Name

Loria Clow

Attorney Docket Number

CHA9 2003 0003 US1

ENCLOSURES (Check all that apply)☐

Fee Transmittal Form

☐

Fee Attached

☐

Amendment/Reply

☐

After Final

☐

Affidavits/declaration(s)

☐

Extension of Time Request

☐

Express Abandonment Request

☐

Information Disclosure Statement

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Certified Copy of Priority Document(s)

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Reply to Missing Parts/Incomplete Application

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Reply to Missing Parts under 37 CFR 1.52 or 1.53

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Drawing(s)

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Petition

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Petition to Convert to a Provisional Application

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After Allowance Communication to TC

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Appeal Communication to Board of Appeals and Interferences

☒

Appeal Communication to TC (Appeal Notice, Brief, Reply Brief)

☐

Proprietary Information

☐

Status Letter

☐

Other Enclosure(s) (please identify below):

Remarks

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm Name

Karl O. Hesse

Signature



Printed name

Karl O. Hesse

Date

October 3, 2007

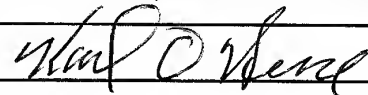
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25,398

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Karl O. Hesse

Date

October 3, 2007

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1 **IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

2
3 Date: October 3, 2007

4
5 In re application of:

6 **Kelkar et al**

7 Serial No.: 10/629,448

8 Filed: July 29, 2003

9 Group Art Unit: 1631

10 Examiner: **Loria Clow**

11 FOR: **Method and Program**

12 **Product for Discovering**

13 **Similar Gene Expression Profiles**

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3 Oct 2007
Date of Signature

14
15
16 **APPEAL BRIEF AND FEE IN SUPPORT OF APPEAL**

17 **FROM THE PRIMARY EXAMINER TO THE BOARD OF APPEALS**

18
19 Assistant Commissioner for Patents

20 Washington DC 20231

21
22 Sir:

23
24 Appellants herewith submit an Appeal Brief in support of the
25 appeal to the Board of Patent Appeals and Interferences from the
26 decision dated May 16, 2007 of the Primary Examiner finally
27 rejecting claims 1-6, 10-16 and 20.

1 **FEE**

2 Please charge the fee of \$510.00 set by 37 CFR § 41.20(b) (2)
3 for filing a brief in support of an appeal to Deposit Account No.
4 09-0469. Charge any excess fee or deposit any overpayment to
5 Deposit Account No. 09-0469.

6
7 **ORAL HEARING**

8 Appellants do not request an Oral Hearing.
9

10 **(1) Real Party in Interest**

11 The real party in interest in this appeal is International
12 Business Machines Corporation, a New York corporation, assignee
13 of the entire right, title and interest in the claimed invention.
14

15 **(2) Related Appeals and Interferences**

16 No other appeals or interferences are known to the
17 Appellants, the Appellants' legal representative, or assignee
18 that will directly affect or be directly affected by or have a
19 bearing on the Board's decision in this appeal.
20

21 **(3) Status of Claims**

22 Claims 1-6, 10-16 and 20 are pending in this application.
23 Claims 7-9 and 17-19 were canceled after restriction.
24 The rejection of claims 10-16 and 20 under 35 U.S.C. 101 and
25 the rejection of claims 1-6 under 35 U.S.C. 101 and
26 for new matter is appealed.
27

28 **(4) Status of Amendments**

29 The amendment filed before final has been entered.
30 The amendment filed after final has not been entered.
31

1 **(5) Summary of Invention**

2 The present invention relates to a method and program
3 product operating in a personal computer for clustering genes
4 having potential functional similarity by a comparison of their
5 time varying gene expression profiles.

6 The method of the invention uses the time and intensity
7 invariant correlation function of the IBM tool to find matches of
8 gene expression profiles using both time and intensity
9 information, which is better at detecting functional similarity
10 than using intensity information alone. The output of
11 Intelligent Miner is a data set of gene expression pairs with the
12 match factor and number of subsets used to compare each pair. A
13 threshold match factor is chosen and genes are listed in clusters
14 by their match fractions. Genes are then removed from all except
15 the cluster with the highest match fraction. Any genes not
16 already in a cluster are added to a cluster which includes a gene
17 that has a highest match fraction with the added gene.

18
19 **(6) Issues**

20
21 I. Whether output to a user is a required claim step in order
22 to define an invention, that is a practical application which is
23 useful, concrete and tangible.

24
25 II. Whether applicants' teaching of a personal computer with
26 implicit, intrinsic and inherent output means in the
27 specification support claims 1 - 6 without adding new matter.
28

Grouping of Claims

With respect to the final rejection of claims 1 - 6, 10 - 16 and 20 under 35 U.S.C. 101, the rejected claims are grouped as 2 groups.

Claim 10 is representative of the group I and is related to Issue I.

Claim 1 is representative of the group II and is related to
Issue II

1 (7) Argument

2
3 **Issue I:** Whether output to a user is a required claim step in
4 order to define an invention, that is a practical application
5 which is useful, concrete and tangible.

6
7 The Group I Claims

8
9 Appellants claim in exemplary claim 10:

10 10. A program product having computer readable code stored on a
11 recordable media for determining similarity between portions of
12 gene expression profiles comprising:

13 programmed means for processing a number of gene expression
14 profiles with a similar sequences algorithm that is a time and
15 intensity invariant correlation function to obtain a data set of
16 gene expression pairs and a match fraction for each pair;

17 programmed means for listing gene expression pairs in
18 clusters by their match fractions;

19 programmed means for removing a first gene from a cluster
20 when the first gene is also in another cluster which has another
21 gene with a higher match fraction with the first gene than any of
22 the genes in the cluster have with the first gene;

23 programmed means for repeating the removing step until all
24 genes are listed in only one cluster.
25

1 Applicants believe that the specification and claims indeed
2 do describe a method and a program product that produce a result
3 that has substantial and credible utility as required by MPEP
4 2107 II and that the claims are limited to a narrow practical
5 application in a computer related art.
6

7 The Examiner relies on the "New Interim Guidelines" to
8 interpret the requirements of the Federal Courts under the
9 current law to require claiming "output to a user". Applicants
10 believe that the Examiner is mistaken and is applying an
11 interpretation of the definition of the word tangible that is:
12 1) narrower than appropriate under the current law and is
13 2) narrower than required under the "New Guidelines".
14

15 1) The introduction to the "New Guidelines" states:
16 "These Examination Guidelines ("Guidelines") are based on the USPTO's current understanding
17 of the law and are believed to be fully consistent with binding precedent of the Supreme Court,
18 the Federal Circuit and the Federal Circuit's predecessor courts. These Guidelines do not
19 constitute substantive rulemaking and hence do not have the force and effect of law."
20

21 In following the "Guidelines", the Examiner appears to
22 require separate interpretations of the words useful, concrete
23 and tangible.
24

25 Applicants' attorney has found no basis in any of the
26 Federal Circuit opinions using these words that imply that these
27 terms are to have separate meanings. They appear to always be
28 used together as synonyms for the concept of being useful and
29 non-abstract. Applicants' attorney has requested that the
30 Examiner provide a citation to a court's requirement that these
31 terms are part of a three pronged test if such is the case in

1 order to help applicants decide whether to appeal or request
2 continued examination. No citation was provided.

3 2) Even under the "Guidelines, the Examiners interpretation
4 of the word tangible is unnecessarily narrow.

5 The "Guidelines" at page 13 recite

6 "Accordingly, a complete definition of the scope of 35 U.S.C. § 101, reflecting Congressional
7 intent, is that any new and useful process, machine, manufacture or composition of matter under
8 the sun that is made by man is the proper subject matter of a patent. The subject matter courts
9 have found to be outside of, or exceptions to, the four statutory categories of invention is limited
10 to abstract ideas, laws of nature and natural phenomena. While this is easily stated, determining
11 whether an applicant is seeking to patent an abstract idea, a law of nature or a natural
12 phenomenon has proven to be challenging."

13
14 Beginning at page 21 the "Guidelines" recite:

15 "TANGIBLE RESULT"

16 "The tangible requirement does not necessarily mean that a claim must either be tied to a particular
17 machine or apparatus or must operate to change articles or materials to a different state or thing.
18 However, the tangible requirement does require that the claim must recite more than a § 101 judicial
19 exception, in that the process claim must set forth a practical application of that § 101 judicial
20 exception to produce a real-world result. Benson, 409 U.S. at 71-72, 175 USPQ at 676-77 (invention
21 ineligible because had "no substantial practical application."). "[A]n application of a law of nature or
22 mathematical formula to a ... process may well be deserving of patent protection." Diehr, 450 U.S.
23 at 187, 209 USPQ at 8 (emphasis added); see also Corning, 56 U.S. (15 How.) at 268, 14 L.Ed. 683
24 ("It is for the discovery or invention of some practical method or means of producing a beneficial
25 result or effect, that a patent is granted ...").

26
27 In other words, the opposite meaning of "tangible" is "abstract."
28 The bare conversion of any binary data as in Gottschalk V. Benson
29 or the bubble sort of any data as in "Warmerdam, 33 F.3d at 1360, 31
30 USPQ2d at 1759 ("steps of 'locating' a medial axis, and 'creating' a bubble hierarchy ... describe

1 nothing more than the manipulation of basic mathematical constructs, the paradigmatic 'abstract
2 idea'")" recited at page 14 of the "Guidelines" are examples of the
3 abstract.
4

5 Applicants' process does not convert or process just any data but
6 is limited to useful concrete and non-abstract gene expression
7 profiles in a data base of such profiles. Applicants' process is
8 but one application of many possible applications of the
9 mathematical steps involved in obtaining the useful result.
10

11 At page 17 of the "Guidelines we see:

12 While abstract ideas, natural phenomena, and laws of nature are not eligible for patenting, methods
13 and products employing abstract ideas, natural phenomena, and laws of nature to perform a real-
14 world function may well be. In evaluating whether a claim meets the requirements of section 101,
15 the claim must be considered as a whole to determine whether it is for a particular application of an
16 abstract idea, natural phenomenon, or law of nature, rather than for the abstract idea, natural
17 phenomenon, or law of nature itself.
18

19 As is clear from the specification and the claim limitations,
20 applicants' process is limited to a particular practical
21 application and is not an abstract idea, natural phenomenon or a
22 law of nature.
23

24 The result is that all of the processed gene expression profiles
25 are each listed in only one cluster. This result of applicants'
26 claims is a very useful, repeatable and non-abstract result which
27 is recognized by those skilled in the medical and computer arts
28 to be of great value and useful, non-abstract and concrete
29 finding of similar gene expression profiles.
30

1 **PRIOR ART**

2 Applicants note that their claims have not been rejected on prior
3 art yet have been restricted on the ground that there were two
4 groups of claims that required two fields of search. It is not
5 apparent whether relevant prior art patents were considered by
6 the Examiner while examining this application. It is believed
7 that the "Guidelines" on page 10 are helpful in determining both
8 the novelty of applicants' invention and the **usefulness and non-**
9 **abstract nature** of applicants' the invention.

10
11 As evidenced by the references which applicants have attempted to
12 incorporate by reference, but have acquiesced to the Examiners
13 correct requirement to cancel, in addition to applicants
14 teachings in the background art section of their specification,
15 users in the medical profession find great value and usefulness
16 in methods for finding similar gene expression profiles that are
17 tangible and concrete. See for example US Patent 6,406,853
18 abstract and claims 25, 26 and US Patent 6,436,642 column 26
19 beginning at line 15.

20
21 It is believed that if the rejections under 35 U.S.C. 101 put
22 forth in this application were appropriate, many of the relevant
23 prior art patents in the appropriate fields of search would be
24 found to be invalid. Since they were issued under the guidance
25 of current statutory law and court cases, it must be that the
26 rejections in this application are based upon excessively narrow
27 and untenable interpretation of the current law.

1 **Issue II:** Whether applicants' teaching of a personal
2 computer with implicit, intrinsic and inherent output means in
3 the specification support claims 1 - 6 without adding new matter.
4

5 The Group II Claims

6 Appellants claim in exemplary claim 1:

7 1. A method for determining similarity between portions of gene
8 expression profiles in a computer comprising the steps of:

9 processing a number of gene expression profiles with a
10 similar sequences algorithm that is a time and intensity
11 invariant correlation function to obtain a data set of gene
12 expression profile pairs and a match fraction for each gene
13 expression profile pair;

14 listing gene expression profile pairs in clusters by their
15 match fractions;

16 removing a first gene expression profile from a cluster when
17 another cluster has another gene expression profile with a higher
18 match fraction with the first gene expression profile, unless the
19 another gene expression profile requires a larger number of
20 subsequences to achieve similarity with the first gene expression
21 profile;

22 repeating the removing step until all gene expression
23 profiles are listed in only one cluster;

24 providing output of the listing of clusters of gene
25 expression profiles.
26

1 Applicants' specification recites: The focal point of the
2 preferred personal computer architecture comprises a processor
3 51. The processor 51 is connected to a bus 52 which comprises a
4 set of data lines, a set of address lines and a set of control
5 lines. A plurality of I/O devices, memory and storage devices
6 53-58 and 66 are connected to the bus 52 through separate
7 adapters 59-64 and 67, respectively. For example, the display 54
8 may be either a CRT or a flat panel display.
9

10 It is believed to be well known in the art as exemplified by
11 prior art patents that users in the medical profession receive
12 output from personal computer input/output devices such as
13 applicants teach in their preferred embodiment. Again,
14 applicants refer to US Patent 6,406,853 abstract and claims 25,
15 26 and US Patent 6,436,642 column 26 beginning at line 15.
16

17 It is believed that material that is implicit, intrinsic, or
18 inherent in the application as filed is not new matter.
19

20 In order to be usable by a user, a personal computer
21 necessarily and constantly exhibits the function of input and
22 output, and such function was recognized as such by those skilled
23 in the art of using personal computers. Therefore applicants'
24 addition of the step of providing such output to satisfy the
25 Examiner's reading of the guidelines was not new matter but is
26 supported in their specification by teachings that are implicit,
27 intrinsic and inherent.
28

1 Accordingly it is believed that the claims are clear,
2 statutory and definite and are drawn to a novel and unobvious
3 method and program product for clustering gene expression
4 profiles which result is concrete, tangible and directly useful
5 in drug selection and disease diagnosis.

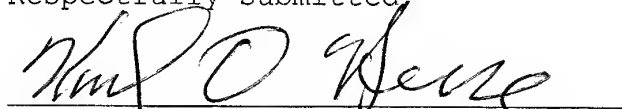
6
7 **Request for Relief**
8

9 Wherefore, Appellants respectfully request that the
10 rejection of pending claims 1 - 6, 10 - 16 and 20 be reversed.
11

12
13
14 Date: October 3, 2007

15 IBM Corporation
16 Intellectual Property Law
17 MG90-201/1
18 8501 IBM Drive
19 Charlotte, NC 28262-8563
20
21
22

Respectfully submitted



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1 **(8) Appendix**

2 **Claims Involved in this Appeal**

3
4 1. A method for determining similarity between portions of
5 gene expression profiles in a computer comprising the steps of:

6 processing a number of gene expression profiles with a
7 similar sequences algorithm that is a time and intensity
8 invariant correlation function to obtain a data set of gene
9 expression profile pairs and a match fraction for each gene
10 expression profile pair;

11 listing gene expression profile pairs in clusters by their
12 match fractions;

13 removing a first gene expression profile from a cluster when
14 another cluster has another gene expression profile with a higher
15 match fraction with the first gene expression profile, unless the
16 another gene expression profile requires a larger number of
17 subsequences to achieve similarity with the first gene expression
18 profile;

19 repeating the removing step until all gene expression
20 profiles are listed in only one cluster;

21 providing output of the listing of clusters of gene
22 expression profiles.
23

1 2. A method for determining similarity between portions of
2 gene expression profiles comprising the steps of:
3 processing a number of gene expression profiles with a
4 similar sequences algorithm that is a time and intensity
5 invariant correlation function to obtain a data set of gene
6 expression pairs and a match fraction for each pair;
7 listing gene expression pairs in clusters by their match
8 fractions;
9 removing a first gene from a first cluster when the first
10 gene is also in a second cluster which has another gene with a
11 higher match fraction with the first gene than any of the genes
12 in the first cluster have with the first gene, but;
13 retaining the first gene in the first cluster and removing
14 the first gene from the second cluster when the difference
15 between the highest match fraction of the first gene with a gene
16 in the first cluster and the highest match fraction of the first
17 gene with a gene in the second cluster is less than a minimum
18 difference threshold and the number of subsequences represented
19 in the similar gene pair having the highest match fraction in the
20 first cluster is higher than the number of subsequences
21 represented in the similar gene pair having the highest match
22 fraction in the second cluster;
23 repeating the removing step until all genes are listed in
24 only one cluster;
25 providing output of the listing of clusters of gene
26 expression profiles.

1 3. A method of determining similarity between portions of
2 gene expression profiles comprising the steps of:
3 processing data embodying a number of gene expression
4 profiles with a similar sequences algorithm in a computer that is
5 a time and intensity invariant correlation function to obtain a
6 data set of gene expression pairs and a match fraction for each
7 pair;
8 choosing a threshold match fraction;
9 listing gene expression pairs in clusters by their match
10 fractions above the threshold;
11 adding each gene not already in a cluster to a cluster
12 having another gene having a highest match fraction with the each
13 gene without regard of the threshold;
14 removing a first gene from a cluster when the first gene is
15 also in another cluster which has another gene with a higher
16 match fraction with the first gene than any of the genes in the
17 cluster have with the first gene;
18 repeating the removing step until all genes are listed in
19 only one cluster;
20 providing output of the listing of clusters of gene
21 expression profiles.

1 4. A method for determining similarity between portions of
2 gene expression profiles comprising the steps of:
3 processing a number of gene expression profiles with a
4 similar sequences algorithm that is a time and intensity
5 invariant correlation function with a computer to obtain a data
6 set of gene expression pairs and a match fraction for each pair;
7 choosing a threshold match fraction;
8 listing gene expression pairs in clusters by their match
9 fractions above the threshold;
10 adding each gene not already in a cluster to a cluster
11 having another gene having a highest match fraction disregarding
12 the threshold with the each gene;
13 removing a first gene from a first cluster when the first
14 gene is also in a second cluster which has another gene with a
15 higher match fraction with the first gene than any of the genes
16 in the first cluster have with the first gene, but;
17 retaining the first gene in the first cluster and removing
18 the first gene from the second cluster when the difference
19 between the highest match fraction of the first gene with a gene
20 in the first cluster and the highest match fraction of the first
21 gene with a gene in the second cluster is less than a minimum
22 difference threshold and the number of subsequences represented
23 in the similar gene pair having the highest match fraction in the
24 first cluster is higher than the number of subsequences
25 represented in the similar gene pair having the highest match
26 fraction in the second cluster;
27 repeating the removing and retaining steps until all genes
28 are listed in only one cluster;
29 providing output of the listing of clusters of gene
30 expression profiles.

1 5. A method in a computer for determining similarity between
2 genes comprising the steps of:
3 listing genes to be compared in a data set by their gene
4 expression profiles;
5 processing the listed gene expression profiles with a
6 similar sequences algorithm that is a time and intensity
7 invariant correlation function to obtain a data set of gene
8 expression pairs and a match fraction for each pair;
9 choosing a threshold match fraction;
10 creating a set G in which to list indices of genes accounted
11 for;
12 assigning genes i and j to a cluster a if they have a match
13 fraction greater than the threshold;
14 assigning gene k to the cluster a if it has a match fraction
15 greater than the threshold with either gene i or gene j;
16 assigning genes k and l to a cluster b if they have a match
17 fraction greater than the threshold and if both gene k and gene l
18 do not have match fractions above the threshold with either gene
19 i or gene j;
20 repeating the assigning steps until all genes to be compared
21 have been considered;
22 removing a first gene from a cluster when another cluster
23 has another gene with a higher match fraction with the first
24 gene;
25 repeating the removing step until all genes are listed in
26 only one cluster;
27 providing output of the listing of clusters of gene
28 expression profiles.
29

1 6. A method in a computer for determining similarity between
2 genes comprising the steps of:
3 listing genes to be compared in a data set by their gene
4 expression profiles;
5 processing the listed gene expression profiles with a
6 similar sequences algorithm that is a time and intensity
7 invariant correlation function to obtain a data set of gene
8 expression pairs and a match fraction for each pair;
9 choosing a threshold match fraction;
10 creating a set G in which to list indices of genes accounted
11 for;
12 assigning genes i and j to cluster 1 if they have a match
13 fraction greater than the threshold;
14 assigning gene k to cluster 1 if it has a match fraction
15 greater than the threshold with either gene i or gene j;
16 assigning genes k and l to cluster 2 if they have a match
17 fraction greater than the threshold and if both gene k and gene l
18 do not have match fractions above the threshold with either gene
19 i or gene j;
20 removing a first gene from a cluster when another cluster
21 has another gene with a higher match fraction with the first
22 gene, unless the another gene requires a larger number of
23 subsequences to achieve similarity with the first gene;
24 repeating the removing step until all genes are listed in
25 only one cluster;
26 providing output of the listing of clusters of gene
27 expression profiles.
28

1 10. A program product having computer readable code stored
2 on a recordable media for determining similarity between portions
3 of gene expression profiles comprising:
4 programmed means for processing a number of gene expression
5 profiles with a similar sequences algorithm that is a time and
6 intensity invariant correlation function to obtain a data set of
7 gene expression pairs and a match fraction for each pair;
8 programmed means for listing gene expression pairs in
9 clusters by their match fractions;
10 programmed means for removing a first gene from a cluster
11 when the first gene is also in another cluster which has another
12 gene with a higher match fraction with the first gene than any of
13 the genes in the cluster have with the first gene;
14 programmed means for repeating the removing step until all
15 genes are listed in only one cluster.

1 11. A program product having computer readable code stored
2 on a recordable media for determining similarity between portions
3 of gene expression profiles using output from a similar sequences
4 algorithm that is a time and intensity invariant correlation
5 function comprising:
6 programmed means for providing a gene expression profile
7 data set as input to programmed means embodying a similar
8 sequences algorithm that is a time and intensity invariant
9 correlation function to obtain a data set of gene expression
10 pairs and a match fraction for each pair as output from the
11 programmed means embodying a similar sequences algorithm;
12 programmed means for listing the gene expression pairs in
13 clusters by their match fractions;
14 programmed means for removing a first gene from a cluster
15 when the first gene is also in another cluster which has another
16 gene with a higher match fraction with the first gene than any of
17 the genes in the cluster have with the first gene;
18 programmed means for repeating the removing step until all
19 genes are listed in only one cluster.

1 12. A program product having computer readable code stored
2 on a recordable media for determining similarity between portions
3 of gene expression profiles comprising the steps of:
4 programmed means for processing a number of gene expression
5 profiles with a similar sequences algorithm that is a time and
6 intensity invariant correlation function to obtain a data set of
7 gene expression pairs and a match fraction for each pair;
8 programmed means for listing gene expression pairs in
9 clusters by their match fractions;
10 programmed means for removing a first gene from a first
11 cluster when the first gene is also in a second cluster which has
12 another gene with a higher match fraction with the first gene
13 than any of the genes in the first cluster have with the first
14 gene, but;
15 programmed means for retaining the first gene in the first
16 cluster and removing the first gene from the second cluster when
17 the difference between the highest match fraction of the first
18 gene with a gene in the first cluster and the highest match
19 fraction of the first gene with a gene in the second cluster is
20 less than a minimum difference threshold and the number of
21 subsequences represented in the similar gene pair having the
22 highest match fraction in the first cluster is higher than the
23 number of subsequences represented in the similar gene pair
24 having the highest match fraction in the second cluster;
25 programmed means for repeating the removing step until all
26 genes are listed in only one cluster.

1 13. A program product having computer readable code stored
2 on a recordable media for determining similarity between portions
3 of gene expression profiles comprising the steps of:

4 programmed means for processing a number of gene expression
5 profiles with a similar sequences algorithm that is a time and
6 intensity invariant correlation function to obtain a data set of
7 gene expression pairs and a match fraction for each pair;

8 programmed means for choosing a threshold match fraction;

9 programmed means for listing gene expression pairs in
10 clusters by their match fractions above the threshold;

11 programmed means for adding each gene not already in a
12 cluster to a cluster having another gene having a highest match
13 fraction with the each gene without regard of the threshold;

14 programmed means for removing a first gene from a cluster
15 when the first gene is also in another cluster which has another
16 gene with a higher match fraction with the first gene than any of
17 the genes in the cluster have with the first gene;

18 programmed means for repeating the removing step until all
19 genes are listed in only one cluster.

1 14. A program product having computer readable code stored
2 on a recordable media for determining similarity between portions
3 of gene expression profiles comprising the steps of:
4 programmed means for processing a number of gene expression
5 profiles with a similar sequences algorithm that is a time and
6 intensity invariant correlation function to obtain a data set of
7 gene expression pairs and a match fraction for each pair;
8 programmed means for choosing a threshold match fraction;
9 programmed means for listing gene expression pairs in
10 clusters by their match fractions above the threshold;
11 programmed means for adding each gene not already in a
12 cluster to a cluster having another gene having a highest match
13 fraction disregarding the threshold with the each gene;
14 programmed means for removing a first gene from a first
15 cluster when the first gene is also in a second cluster which has
16 another gene with a higher match fraction with the first gene
17 than any of the genes in the first cluster have with the first
18 gene, but;
19 programmed means for retaining the first gene in the first
20 cluster and removing the first gene from the second cluster when
21 the difference between the highest match fraction of the first
22 gene with a gene in the first cluster and the highest match
23 fraction of the first gene with a gene in the second cluster is
24 less than a minimum difference threshold and the number of
25 subsequences represented in the similar gene pair having the
26 highest match fraction in the first cluster is higher than the
27 number of subsequences represented in the similar gene pair
28 having the highest match fraction in the second cluster;
29 programmed means for repeating the removing and retaining
30 steps until all genes are listed in only one cluster.

1 15. A program product having computer readable code stored
2 on a recordable media for determining similarity between genes
3 comprising the steps of:
4 programmed means for listing genes to be compared by their
5 gene expression profiles;
6 programmed means for processing the listed gene expression
7 profiles with a similar sequences algorithm that is a time and
8 intensity invariant correlation function to obtain a data set of
9 gene expression pairs and a match fraction for each pair;
10 programmed means for choosing a threshold match fraction;
11 programmed means for creating a null set $G(0)$ to hold genes
12 accounted for;
13 programmed means for assigning genes i and j to cluster 1 if
14 they have a match fraction greater than the threshold;
15 programmed means for assigning gene k to cluster 1 if it has
16 a match fraction greater than the threshold with either gene i or
17 gene j ;
18 programmed means for assigning genes k and l to cluster 2 if
19 they have a match fraction greater than the threshold and if both
20 gene k and gene l do not have match fractions above the threshold
21 with either gene i or gene j ;
22 programmed means for removing a first gene from a cluster
23 when another cluster has another gene with a higher match
24 fraction with the first gene;
25 programmed means for repeating the removing step until all
26 genes are listed in only one cluster.
27

1 16. A program product having computer readable code stored
2 on a recordable media for determining similarity between genes
3 comprising the steps of:
4 programmed means for listing genes to be compared by their
5 gene expression profiles;
6 programmed means for processing the listed gene expression
7 profiles with a similar sequences algorithm that is a time and
8 intensity invariant correlation function to obtain a data set of
9 gene expression pairs and a match fraction for each pair;
10 programmed means for choosing a threshold match fraction;
11 programmed means for creating a null set $G(0)$ to hold genes
12 accounted for;
13 programmed means for assigning genes i and j to cluster 1 if
14 they have a match fraction greater than the threshold;
15 programmed means for assigning gene k to cluster 1 if it has
16 a match fraction greater than the threshold with either gene i or
17 gene j ;
18 programmed means for assigning genes k and l to cluster 2 if
19 they have a match fraction greater than the threshold and if both
20 gene k and gene l do not have match fractions above the threshold
21 with either gene i or gene j ;
22 programmed means for removing a first gene from a cluster
23 when another cluster has another gene with a higher match
24 fraction with the first gene, unless the another gene requires a
25 larger number of subsequences to achieve similarity with the
26 first gene;
27 programmed means for repeating the removing step until all
28 genes are listed in only one cluster.
29

1 20. In a method of determining similarity between portions
2 of gene expression profiles which includes processing a number of
3 gene expression profiles using a computer with a similar
4 sequences algorithm that is a time and intensity invariant
5 correlation function to obtain a data set of gene expression
6 pairs and a match fraction for each pair, the improvement
7 comprising the steps of:

8 listing gene expression pairs in clusters by their match
9 fractions;

10 removing a first gene from a cluster when another cluster
11 has another gene with a higher match fraction with the first
12 gene, unless the another gene requires a larger number of
13 subsequences to achieve similarity with the first gene;

14 repeating the removing step until all genes are listed in
15 only one cluster;

16 providing output of the listing of clusters of gene
17 expression profiles.

18